RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/574,129
Source: IFWP
Date Processed by STIC: 9-13-06

ENTERED

IFWP

RAW SEQUENCE LISTING   DATE: 04/13/2006
PATENT APPLICATION: US/10/574,129   TIME: 10:02:54

Input Set : F:\180-179 PCT.ST25.txt
Output Set: N:\CRF4\04132006\J574129.raw

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 3 <110> APPLICANT: Li, Chuan-Yuan
 4         Zhang, Xiuwu
 5         Dewhirst, Mark W
 7 <120> TITLE OF INVENTION: A NOVEL siRNA-BASED APPROACH TO TARGET THE HIF-ALPHA FACTOR
FOR
 8         GENE THERAPY
10 <130> FILE REFERENCE: 180-179 PCT
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/574,129
C--> 12 <141> CURRENT FILING DATE: 2006-03-31
12 <150> PRIOR APPLICATION NUMBER: US 60/508,145
13 <151> PRIOR FILING DATE: 2003-10-02
15 <160> NUMBER OF SEQ ID NOS: 12
17 <170> SOFTWARE: PatentIn version 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3958
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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26 <221> NAME/KEY: CDS
27 <222> LOCATION: (285)..(2765)
29 <400> SEQUENCE: 1
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34 ttgccgcccg cttctctcta gtctcacgag gggtttcccg cctcgcaccc ccacctctgg     180
36 acttgccttt ccttctcttc tccgcgtgtg gagggagcca gcgcttaggc cggagcgagc     240
38 ctgggggccg cccgccgtga agacatcgcg gggaccgatt cacc atg gag ggc gcc     296
39                                                    Met Glu Gly Ala
40                                                    1
42 ggc ggc gcg aac gac aag aaa aag ata agt tct gaa cgt cga aaa gaa      344
43 Gly Gly Ala Asn Asp Lys Lys Lys Ile Ser Ser Glu Arg Arg Lys Glu
44 5               10                  15                  20
46 aag tct cga gat gca gcc aga tct cgg cga agt aaa gaa tct gaa gtt      392
47 Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Lys Glu Ser Glu Val
48             25                  30                  35
50 ttt tat gag ctt gct cat cag ttg cca ctt cca cat aat gtg agt tcg      440
51 Phe Tyr Glu Leu Ala His Gln Leu Pro Leu Pro His Asn Val Ser Ser
52         40                  45                  50
54 cat ctt gat aag gcc tct gtg atg agg ctt acc atc agc tat ttg cgt      488
55 His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile Ser Tyr Leu Arg
56         55                  60                  65
58 gtg agg aaa ctt ctg gat gct ggt gat ttg gat att gaa gat gac atg      536
59 Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile Glu Asp Asp Met
60     70                  75                  80
62 aaa gca cag atg aat tgc ttt tat ttg aaa gcc ttg gat ggt ttt gtt      584
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63 Lys Ala Gln Met Asn Cys Phe Tyr Leu Lys Ala Leu Asp Gly Phe Val
64 85                  90              95                 100
66 atg gtt ctc aca gat gat ggt gac atg att tac att tct gat aat gtg      632
67 Met Val Leu Thr Asp Asp Gly Asp Met Ile Tyr Ile Ser Asp Asn Val
68             105                 110                 115
70 aac aaa tac atg gga tta act cag ttt gaa cta act gga cac agt gtg      680
71 Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr Gly His Ser Val
72             120                 125                 130
74 ttt gat ttt act cat cca tgt gac cat gag gaa atg aga gaa atg ctt      728
75 Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met Arg Glu Met Leu
76         135                 140                 145
78 aca cac aga aat ggc ctt gtg aaa aag ggt aaa gaa caa aac aca cag      776
79 Thr His Arg Asn Gly Leu Val Lys Lys Gly Lys Glu Gln Asn Thr Gln
80      150                 155                 160
82 cga agc ttt ttt ctc aga atg aag tgt acc cta act agc cga gga aga      824
83 Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr Ser Arg Gly Arg
84 165                 170                 175                 180
86 act atg aac ata aag tct gca aca tgg aag gta ttg cac tgc aca ggc      872
87 Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu His Cys Thr Gly
88             185                 190                 195
90 cac att cac gta tat gat acc aac agt aac caa cct cag tgt ggg tat      920
91 His Ile His Val Tyr Asp Thr Asn Ser Asn Gln Pro Gln Cys Gly Tyr
92             200                 205                 210
94 aag aaa cca cct atg acc tgc ttg gtg ctg att tgt gaa ccc att cct      968
95 Lys Lys Pro Pro Met Thr Cys Leu Val Leu Ile Cys Glu Pro Ile Pro
96          215                 220                 225
98 cac cca tca aat att gaa att cct tta gat agc aag act ttc ctc agt     1016
99 His Pro Ser Asn Ile Glu Ile Pro Leu Asp Ser Lys Thr Phe Leu Ser
100      230                 235                 240
102 cga cac agc ctg gat atg aaa ttt tct tat tgt gat gaa aga att acc    1064
103 Arg His Ser Leu Asp Met Lys Phe Ser Tyr Cys Asp Glu Arg Ile Thr
104 245                 250                 255                 260
106 gaa ttg atg gga tat gag cca gaa gaa ctt tta ggc cgc tca att tat    1112
107 Glu Leu Met Gly Tyr Glu Pro Glu Glu Leu Leu Gly Arg Ser Ile Tyr
108             265                 270                 275
110 gaa tat tat cat gct ttg gac tct gat cat ctg acc aaa act cat cat    1160
111 Glu Tyr Tyr His Ala Leu Asp Ser Asp His Leu Thr Lys Thr His His
112             280                 285                 290
114 gat atg ttt act aaa gga caa gtc acc aca gga cag tac agg atg ctt    1208
115 Asp Met Phe Thr Lys Gly Gln Val Thr Thr Gly Gln Tyr Arg Met Leu
116         295                 300                 305
118 gcc aaa aga ggt gga tat gtc tgg gtt gaa act caa gca act gtc ata    1256
119 Ala Lys Arg Gly Gly Tyr Val Trp Val Glu Thr Gln Ala Thr Val Ile
120      310                 315                 320
122 tat aac acc aag aat tct caa cca cag tgc att gta tgt gtg aat tac    1304
123 Tyr Asn Thr Lys Asn Ser Gln Pro Gln Cys Ile Val Cys Val Asn Tyr
124 325                 330                 335                 340
126 gtt gtg agt ggt att att cag cac gac ttg att ttc tcc ctt caa caa    1352
127 Val Val Ser Gly Ile Ile Gln His Asp Leu Ile Phe Ser Leu Gln Gln
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128                345              350              355
130 aca gaa tgt gtc ctt aaa ccg gtt gaa tct tca gat atg aaa atg act     1400
131 Thr Glu Cys Val Leu Lys Pro Val Glu Ser Ser Asp Met Lys Met Thr
132                360              365              370
134 cag cta ttc acc aaa gtt gaa tca gaa gat aca agt agc ctc ttt gac     1448
135 Gln Leu Phe Thr Lys Val Glu Ser Glu Asp Thr Ser Ser Leu Phe Asp
136                375              380              385
138 aaa ctt aag aag gaa cct gat gct tta act ttg ctg gcc cca gcc gct     1496
139 Lys Leu Lys Lys Glu Pro Asp Ala Leu Thr Leu Leu Ala Pro Ala Ala
140     390              395              400
142 gga gac aca atc ata tct tta gat ttt ggc agc aac gac aca gaa act     1544
143 Gly Asp Thr Ile Ile Ser Leu Asp Phe Gly Ser Asn Asp Thr Glu Thr
144 405              410              415              420
146 gat gac cag caa ctt gag gaa gta cca tta tat aat gat gta atg ctc     1592
147 Asp Asp Gln Gln Leu Glu Glu Val Pro Leu Tyr Asn Asp Val Met Leu
148                425              430              435
150 ccc tca ccc aac gaa aaa tta cag aat ata aat ttg gca atg tct cca     1640
151 Pro Ser Pro Asn Glu Lys Leu Gln Asn Ile Asn Leu Ala Met Ser Pro
152                440              445              450
154 tta ccc acc gct gaa acg cca aag cca ctt cga agt agt gct gac cct     1688
155 Leu Pro Thr Ala Glu Thr Pro Lys Pro Leu Arg Ser Ser Ala Asp Pro
156     455              460              465
158 gca ctc aat caa gaa gtt gca tta aaa tta gaa cca aat cca gag tca     1736
159 Ala Leu Asn Gln Glu Val Ala Leu Lys Leu Glu Pro Asn Pro Glu Ser
160     470              475              480
162 ctg gaa ctt tct ttt acc atg ccc cag att cag gat cag aca cct agt     1784
163 Leu Glu Leu Ser Phe Thr Met Pro Gln Ile Gln Asp Gln Thr Pro Ser
164 485              490              495              500
166 cct tcc gat gga agc act aga caa agt tca cct gag cct aat agt ccc     1832
167 Pro Ser Asp Gly Ser Thr Arg Gln Ser Ser Pro Glu Pro Asn Ser Pro
168                505              510              515
170 agt gaa tat tgt ttt tat gtg gat agt gat atg gtc aat gaa ttc aag     1880
171 Ser Glu Tyr Cys Phe Tyr Val Asp Ser Asp Met Val Asn Glu Phe Lys
172                520              525              530
174 ttg gaa ttg gta gaa aaa ctt ttt gct gaa gac aca gaa gca aag aac     1928
175 Leu Glu Leu Val Glu Lys Leu Phe Ala Glu Asp Thr Glu Ala Lys Asn
176                535              540              545
178 cca ttt tct act cag gac aca gat tta gac ttg gag atg tta gct ccc     1976
179 Pro Phe Ser Thr Gln Asp Thr Asp Leu Asp Leu Glu Met Leu Ala Pro
180     550              555              560
182 tat atc cca atg gat gat gac ttc cag tta cgt tcc ttc gat cag ttg     2024
183 Tyr Ile Pro Met Asp Asp Asp Phe Gln Leu Arg Ser Phe Asp Gln Leu
184 565              570              575              580
186 tca cca tta gaa agc agt tcc gca agc cct gaa agc gca agt cct caa     2072
187 Ser Pro Leu Glu Ser Ser Ser Ala Ser Pro Glu Ser Ala Ser Pro Gln
188                585              590              595
190 agc aca gtt aca gta ttc cag cag act caa ata caa gaa cct act gct     2120
191 Ser Thr Val Thr Val Phe Gln Gln Thr Gln Ile Gln Glu Pro Thr Ala
192                600              605              610
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195 Asn Ala Thr Thr Thr Thr Ala Thr Thr Asp Glu Leu Lys Thr Val Thr
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198 aaa gac cgt atg gaa gac att aaa ata ttg att gca tct cca tct cct        2216
199 Lys Asp Arg Met Glu Asp Ile Lys Ile Leu Ile Ala Ser Pro Ser Pro
200     630                 635                 640
202 acc cac ata cat aaa gaa act act agt gcc aca tca tca cca tat aga        2264
203 Thr His Ile His Lys Glu Thr Thr Ser Ala Thr Ser Ser Pro Tyr Arg
204 645                 650                 655                 660
206 gat act caa agt cgg aca gcc tca cca aac aga gca gga aaa gga gtc        2312
207 Asp Thr Gln Ser Arg Thr Ala Ser Pro Asn Arg Ala Gly Lys Gly Val
208             665                 670                 675
210 ata gaa cag aca gaa aaa tct cat cca aga agc cct aac gtg tta tct        2360
211 Ile Glu Gln Thr Glu Lys Ser His Pro Arg Ser Pro Asn Val Leu Ser
212         680                 685                 690
214 gtc gct ttg agt caa aga act aca gtt cct gag gaa gaa cta aat cca        2408
215 Val Ala Leu Ser Gln Arg Thr Thr Val Pro Glu Glu Glu Leu Asn Pro
216         695                 700                 705
218 aag ata cta gct ttg cag aat gct cag aga aag cga aaa atg gaa cat        2456
219 Lys Ile Leu Ala Leu Gln Asn Ala Gln Arg Lys Arg Lys Met Glu His
220     710                 715                 720
222 gat ggt tca ctt ttt caa gca gta gga att gga aca tta tta cag cag        2504
223 Asp Gly Ser Leu Phe Gln Ala Val Gly Ile Gly Thr Leu Leu Gln Gln
224 725                 730                 735                 740
226 cca gac gat cat gca gct act aca tca ctt tct tgg aaa cgt gta aaa        2552
227 Pro Asp Asp His Ala Ala Thr Thr Ser Leu Ser Trp Lys Arg Val Lys
228             745                 750                 755
230 gga tgc aaa tct agt gaa cag aat gga atg gag caa aag aca att att        2600
231 Gly Cys Lys Ser Ser Glu Gln Asn Gly Met Glu Gln Lys Thr Ile Ile
232         760                 765                 770
234 tta ata ccc tct gat tta gca tgt aga ctg ctg ggg caa tca atg gat        2648
235 Leu Ile Pro Ser Asp Leu Ala Cys Arg Leu Leu Gly Gln Ser Met Asp
236         775                 780                 785
238 gaa agt gga tta cca cag ctg acc agt tat gat tgt gaa gtt aat gct        2696
239 Glu Ser Gly Leu Pro Gln Leu Thr Ser Tyr Asp Cys Glu Val Asn Ala
240     790                 795                 800
242 cct ata caa ggc agc aga aac cta ctg cag ggt gaa gaa tta ctc aga        2744
243 Pro Ile Gln Gly Ser Arg Asn Leu Leu Gln Gly Glu Glu Leu Leu Arg
244 805                 810                 815                 820
246 gct ttg gat caa gtt aac tga gctttttctt aatttcattc cttttttggg        2795
247 Ala Leu Asp Gln Val Asn
248             825
250 acactggtgg ctcactacct aaagcagtct atttatattt tctacatcta attttagaag        2855
252 cctggctaca atactgcaca aacttggtta gttcaatttt tgatcccctt tctacttaat        2915
254 ttacattaat gctctttttt agtatgttct ttaatgctgg atcacagaca gctcattttc        2975
256 tcagtttttt ggtatttaaa ccattgcatt gcagtagcat cattttaaaa aatgcacctt        3035
258 tttatttatt tattttggc tagggagttt atcccttttt cgaattattt ttaagaagat         3095
260 gccaatataa ttttgtaag aaggcagtaa cctttcatca tgatcatagg cagttgaaaa         3155
262 attttttacac cttttttttc acattttaca taaataataa tgctttgcca gcagtacgtg        3215
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268 acctggaaca tgacattgtt aatcatataa taatgattct taaatgctgt atggtttatt 3395
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272 gtggcattta tttggataaa attctcaatt cagagaaatc atctgatgtt tctatagtca 3515
274 ctttgccagc tcaaaagaaa acaataccct atgtagttgt ggaagtttat gctaatattg 3575
276 tgtaactgat attaaaccta aatgttctgc ctaccctgtt ggtataaaga tattttgagc 3635
278 agactgtaaa caagaaaaaa aaaatcatgc attcttagca aaattgccta gtatgttaat 3695
280 ttgctcaaaa tacaatgttt gattttatgc actttgtcgc tattaacatc ctttttttca 3755
282 tgtagatttc ataattgag taattttaga agcattattt taggaatata tagttgtcac 3815
284 agtaaatatc ttgttttttc tatgtacatt gtacaaattt ttcattcctt ttgctctttg 3875
286 tggttggatc taacactaac tgtattgttt tgttacatca aataaacatc ttctgtggac 3935
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292 <211> LENGTH: 826
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307         35                  40                  45
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311     50                  55                  60
314 Ser Tyr Leu Arg Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile
315 65                  70                  75                  80
318 Glu Asp Asp Met Lys Ala Gln Met Asn Cys Phe Tyr Leu Lys Ala Leu
319             85                  90                  95
322 Asp Gly Phe Val Met Val Leu Thr Asp Asp Gly Asp Met Ile Tyr Ile
323             100                 105                 110
326 Ser Asp Asn Val Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr
327         115                 120                 125
330 Gly His Ser Val Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met
331     130                 135                 140
334 Arg Glu Met Leu Thr His Arg Asn Gly Leu Val Lys Lys Gly Lys Glu
335 145                 150                 155                 160
338 Gln Asn Thr Gln Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr
339             165                 170                 175
342 Ser Arg Gly Arg Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu
343             180                 185                 190
346 His Cys Thr Gly His Ile His Val Tyr Asp Thr Asn Ser Asn Gln Pro
347         195                 200                 205
350 Gln Cys Gly Tyr Lys Lys Pro Pro Met Thr Cys Leu Val Leu Ile Cys
351     210                 215                 220
354 Glu Pro Ile Pro His Pro Ser Asn Ile Glu Ile Pro Leu Asp Ser Lys
355 225                 230                 235                 240
358 Thr Phe Leu Ser Arg His Ser Leu Asp Met Lys Phe Ser Tyr Cys Asp
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 20,21,22,23,24,25,26,27,28,48,49,50,51,52,53,54,55

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,8

VERIFICATION SUMMARY   DATE: 04/13/2006
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0